

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2000, 07:25:40 ; Search time 727.75 Seconds
(without alignments)
2735.846 Million cell updates/sec

Title: US-09-227-881-1

Perfect score: 5300

Sequence: 1 attcttctcagtttaccctc.....caggcactctcagcacagc 5300

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_36:*

- 1: /cgn2_2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
- 2: /cgn2_2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
- 3: /cgn2_2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
- 4: /cgn2_2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
- 5: /cgn2_2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
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- 20: /cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
- 21: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5299	100.0	5300	19	Human TIGR promote
2	5298.4	100.0	5300	19	Human TIGR promote
3	5298.4	100.0	5300	19	Human TIGR promote
4	5298.4	100.0	5300	19	Human TIGR promote
5	5298.4	100.0	5300	19	Human TIGR promote
6	5298.4	100.0	5300	19	Human TIGR promote
7	5298.4	100.0	5300	19	Human TIGR promote
8	5275.4	99.5	6169	19	Human TIGR upstre
9	1858	35.1	2800	21	Human GLCIA gene e
10	176.4	3.3	283	15	AP2 sequence obtd.
11	175.2	3.3	162450	21	Retinoblastoma bin
12	174.2	3.3	282	18	Consensus Alu repe

c 13	173.6	3.3	17327	14	044278	Serglycin - proteo
c 14	173.2	3.3	49999	20	223900	Human LOBO homolog
c 15	172.8	3.3	452	17	T42809	Polymorphic locus
c 16	172.8	3.3	106746	21	A10225	Human PCTA-1 genom
c 17	172	3.2	2932	13	Q25388	TXA2 receptor gene
c 18	172	3.2	2932	20	232161	Human thromboxane
c 19	172	3.2	2932	20	232162	Human endothelial
c 20	172	3.2	43069	20	236335	Genomic sequence o
c 21	171.6	3.2	10380	18	T67164	Human alpha-N-acet
c 22	171.2	3.2	21721	20	X83427	Human lipoLysis st
c 23	171.2	3.2	22976	20	X83426	Genomic region con
c 24	171	3.2	54548	21	245596	DNA sequence of th
c 25	170.8	3.2	2617	21	AD3452	cDNA encoding huma
c 26	170.4	3.2	3234	16	Q92781	Human thymopoietin
c 27	170	3.2	15056	19	V52967	Human thymopoietin
c 28	170	3.2	15056	21	V29933	DNA sequence of co
c 29	169.6	3.2	2426	21	A06689	Human Immunogenic
c 30	169	3.2	5543	18	T75284	Nucleotide sequenc
c 31	168.4	3.2	11288	16	Q90512	CEA clone HindIII-
c 32	168.2	3.2	3089	21	264958	Membrane-bound pro
c 33	167.4	3.2	555	20	V90098	EST clone CW1682.
c 34	167.4	3.2	41783	21	A35029	Human adenosine re
c 35	167.4	3.2	138169	21	A34791	Human adenosine re
c 36	167.4	3.2	141589	21	A35005	Human adenosine re
c 37	167.4	3.2	141589	21	A35030	Human adenosine re
c 38	167.4	3.2	162450	21	286967	Retinoblastoma bin
c 39	166.8	3.1	7849	16	Q94109	bHL genomic DNA.
c 40	166.4	3.1	1601	21	A35191	Human adenosine re
c 41	166.4	3.1	1601	21	246814	Interleukin-10 (IL
c 42	166.4	3.1	166.4	12	Q10207	p15C insert conta
c 43	166.4	3.1	1618	14	Q46958	Human cytokine syn
c 44	166.4	3.1	1618	21	286905	Human CSIF coding
c 45	166.4	3.1	1645	21	258659	Human Interleukin-

ALIGNMENTS

RESULT	ID	Description
1	V51361	standard; DNA; 5299 BP.
AC	V51361:	
XX		
DT	27-OCT-1998	(first entry)
XX		
DE	Human TIGR promoter region DNA.	
XX		
KW	TIGR: trabecular meshwork induced glucocorticoid response protein; human;	
KW	diagnosis; glaucoma; polymorphism; steroid sensitivity; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	W09832850-A1.	
XX		
PD	30-JUL-1998.	
XX		
PF	09-JAN-1998; 98WO-US00468.	
XX		
PR	26-SEP-1997; 97US-0938669.	
XX		
PR	28-JAN-1997; 97US-0791154.	
XX		
PA	(REGC) UNIV CALIFORNIA.	
XX		
PI	Chen H, Chen P, Nguyen TD, Polansky JR;	
XX		
DR	WPI; 1998-427946/36.	
XX		
PT	Use of TIGR nucleic acid sequences - used for, e.g. developing	
XX		
PT	products for diagnosis, prognosis and treatment of glaucoma	
XX		
PS	Claim 34; Fig 1; 105bp; English.	
XX		

CC This sequence is a trabecular meshwork induced glucocorticoid response
CC protein (TIGR) promoter region which is used in a method for diagnosing
CC glaucoma in a patient. The method involves the detection of polymorphisms
CC whose presence is predictive of a mutation affecting TIGR response in the
CC patient and can be diagnostic of glaucoma or steroid sensitivity. Base
CC substitutions and base additions upstream of and within TIGR exons can
CC also be used to diagnose glaucoma.

XX Sequence 5299 BP; 1482 A; 1151 C; 1235 G; 1431 T; 0 other;

Query Match 100.0%; Score 5299; DB 19; Length 5299;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 attcttctcgtttactctcaggcgtattatgtaaatgaaatgagataaccatgtgaaag 60
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Dp	2101	ccctacctctgtgaggtgtgaacagttctctatgtgaagaagctgtcagaaagaataatgaacaa	2160
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Dp	2581	gctgtcccaagatgtctcaagtggtgtgtgtctcaacggggcgctgtgagagtttcctgtctctccctgtgagc	2640
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Dp	2701	ataaagctcagatctgtataaatcaaatccaaggtgtgtcactgtgtgtttctctccatcagaagagccttat	2760
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Dp	2761	ttaaattgggaataataggaagagagatcgaattctccaaagccgttaattccaacgaagaagatgtac	2820
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Dp	2821	tggagctcttctctctcaatgtctctctgtggcaactactcaagccctgtgtgtgagactgtgtctta	2880
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Dp	3001	ataaagaacctgtcagactctcgtgtctctgtgtgaacactctccctgtgactctctctgtgtgaagg	3060

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Db	3781	taaaagccaaaacagatctcaagcctagatctgtctgactataatgatactggttttttgaaaaat	3840
QY	3841	catttcagcgatgtgttctctctctgattccagaaatgagacgtgtaccccttggccaagctg	3900
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[illegible]

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Db 5221 gctcccagatataataaacctcttgagcctcggtcgtatgacgacgaagccaccatc 5280
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Db 5281 cagcacctctcagcacag 5299

RESULT 2
ID V51362 standard; DNA: 5300 BP.
AC V51362:
XX 27-OCT-1998 (first entry)
DE Human TIGR promoter mutant TIGRm1 DNA.
XX
XX TIGR: trabecular meshwork induced glucocorticoid response protein; human;
KW diagnosis: glaucoma; polymorphism; steroid sensitivity; mutant; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH mutation 4337
FT /tag= a
FT /note= "wild type C is replaced by G"
FT
PN WO9832850-A1.
XX
XX 30-JUL-1998.
PD
XX
XX 09-JAN-1998; 98WO-US00468.
PF
XX 26-SEP-1997; 97US-0938669.
PR 28-JAN-1997; 97US-0791154.
XX
XX (REGC ) UNIV CALIFORNIA.
PA
PI Chen H, Chen P, Nguyen TD, Polansky JR;
XX
XX WPI: 1998-427946/36.
DR
XX
XX Use of TIGR nucleic acid sequences - used for, e.g. developing
PT products for diagnosis, prognosis and treatment of glaucoma
PI
XX
XX Disclosure: Fig 2; 105pp; English.
XX
XX This sequence is a trabecular meshwork induced glucocorticoid response
CC protein (TIGR) promoter mutant, TIGRm1, which is used in a method for
CC diagnosing glaucoma in a patient. The method involves the detection of
CC polymorphisms whose presence is predictive of a mutation affecting TIGR
CC response in the patient and can be diagnostic of glaucoma or steroid
CC sensitivity. Base substitutions and base additions upstream of and within
CC TIGR exons can also be used to diagnose glaucoma.
XX
SQ Sequence 5300 BP; 1482 A; 1151 C; 1236 G; 1431 T; 0 other;

Query Match 100.0%; Score 5298.4; DB 19; Length 5300;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy 961 tttaagacatgagctcccaatttataaagtcagagcatatacagagataacgctgccagctcc 1020
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Oy 1141 gggcctcaaacatctgttaacgtgtcatctccagtaggtcccatatacaaatgcccacccccc 1200
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Dp	2401	ccagaaagagaaatcgaaagagaaagaaacagctcaaaacgaaagaaatctcgaaagagaaagctgttc	2460
Qy	2461	ctcagagagaaagagagcgtcccaacgctcccaagagaaatctcaagaggtcgagagctcgaaagag	2520
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Qy	4441	ctttgaaatagacacctcctgtcgtgatactctgtgttttaaaatacttaataaacaatgtttaa	4500
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Qy	4501	attttgatactttgtaatacataattcaattcaatctgttccctctgtacatataattt	4560
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[illegible]

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XX
XX      30-JUL-1998.
XX
XX      09-JAN-1998; 98WO-US00468.
XX
XX      26-SEP-1997; 97US-0938659.
XX      28-JAN-1997; 97US-0791154.
XX
XX      (REGC ) UNIV CALIFORNIA.
XX
XX      Chen H, Chen P, Nguyen TD, Polansky JR;
XX      WPI: 1998-427946/36.
XX
XX      Use of TIGR nucleic acid sequences - used for, e.g. developing
XX      products for diagnosis, prognosis and treatment of glaucoma
XX
XX      Disclosure: Fig 2, 105pp: English.
XX
XX      This sequence is a trabecular meshwork induced glucocorticoid response
XX      protein (TIGR) promoter mutant, TIGRmt2, which is used in a method for
XX      diagnosing glaucoma in a patient. The method involves the detection of
XX      polymorphisms whose presence is predictive of a mutation affecting TIGR
XX      response in the patient and can be diagnostic of glaucoma or steroid
XX      sensitivity. Base substitutions and base additions upstream of and within
XX      TIGR exons can also be used to diagnose glaucoma.
XX
XX      Sequence 5300 BP; 1482 A; 1151 C; 1235 G; 1432 T; 0 other;
XX

```

RESULT	3
V51363	
ID	V51363 standard; DNA: 5300 BP.
XX	
AC	V51363:
XX	
DT	27-OCT-1998 (first entry)
XX	
DE	Human TIGR promoter mutant TIGRmt2 DNA.
XX	
KW	TIGR: trabecular meshwork induced glucocorticoid response protein; human; diagnosis: glaucoma; polymorphism; steroid sensitivity; mutant; ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
XX	
Key	
FT	Location/Qualifiers
mutation	4950

	Query Match	Similarity	100.0%	Score 5298.4	DB 19	Length 5300:	
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Dd	301	gagagaagaataatgagaaaataaaactttcccttgtttttaatttcaggagaaaaatg	360				
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D	4801	ctgtgtctcggcgtgctgttatatttctctctgctccctgcagcttcaagaagcctgttt	4860
Q	4861	ggatctccagttctcagcagatgagtcgctggcagagttcccaatgagttctgcagag	4920
D	4861	ggatctccagttctcagcagatgagtcgctggcagagttcccaatgagttctgcagag	4920
Q	4921	tgaatggaataataaacatagaataataatcctgtgtgaatcagcacacagtagtccgtg	4980
D	4921	tgaatggaataataaacatagaataataatcctgtgtgaatcagcacacagtagtccgtg	4980
Q	4981	tgtaagatgtgtgtaagtggt	5040
D	4981	tgtaagatgtgtgtaagtggt	5040
Q	5041	taggaacttatattgaggt	5100
D	5041	taggaacttatattgaggt	5100
Q	5101	caaacagactcttggaaggtatttcttaagaaatctgtctgagcaggtggaagcaacccc	5160
D	5101	caaacagactcttggaaggtatttcttaagaaatctgtctgagcaggtggaagcaacccc	5160
Q	5161	cctgtgcaagccccacacagcctcaagctgagccactctctcccccctgaagggctg	5220
D	5161	cctgtgcaagccccacacagcctcaagctgagccactctctcccccctgaagggctg	5220
Q	5221	gtcccccagatataataaacctctctgagagctcgggcatgagccagcaagccacacatc	5280
D	5221	gtcccccagatataataaacctctctgagagctcgggcatgagccagcaagccacacatc	5280

[illegible]

Db	2341	gctctgcgttcccgctgaatcgtcttcgtgtcatctctgagcctgcggagacccttgctgtccagagct	2400
Oy	2401	ccagaaagagaaatcggagagcggaacatagctctaaacggagaaatcttgagagggagacagtcttc	2460
Db	2401	ccagaaagagaaatcggagagcggaacatagctctaaacggagaaatcttgagagggagacagtcttc	2460
Oy	2461	ctcaagagggaaaggggctctccacgtcccaaggagaaatctccagagagtggtgggagctgcagggag	2520
Db	2461	ctcaagagggaaaggggctctccacgtcccaaggagaaatctccagagagtggtgggagctgcagggag	2520
Oy	2521	tggggagcgtctggagctctgagcgggtgtcctgaagagcggagagtgtaaaagggcagagctgaa	2580
Db	2521	tggggagcgtctggagcgtctgagcgggtgtcctgaagagcggagagtgtaaaagggcagagctgaa	2580
Oy	2581	gctgcgcagagtgctcagtgctgtctcaacgggctctggagcttcctcgcttcctctgtagac	2640
Db	2581	gctgcgcagagtgctcagtgctgtctcaacgggctctggagcttcctcgcttcctctctgtagac	2640
Oy	2641	cttttatctttcttcctgtcttgagaggaagagagcttatctcaatgaagagagcagcttc	2700
Db	2641	cttttatctttcttcctctctctgagaggaagagagcttatctcaatgaagagagcagcttc	2700
Oy	2701	ataaagctcagctgtttaaaatctcaagagtggtgatgtgtttctctcaagaaagccttat	2760
Db	2701	ataaagctcagctgttaaaatctcaagagtggtgatgtgtttctctcaagaaagcctttat	2760
Oy	2761	ttaatctggagaaataaagaaagcgaagctcatctccctaaagccgttaatcacggaagagtgac	2820
Db	2761	ttaatctggagaaataaagaaagcgaagctcatctccctaaagccgttaatcacggaagagtgac	2820
Oy	2821	tggagctttttctttcttcacagtctctcgggacactactcaagcccttggtgggtacttgctta	2880
Db	2821	tggagctttctttcttcacagtctctcgggacactactcaagcccttggtgggtacttgctta	2880
Oy	2881	tgcagagacgctcgaagaccttgaaatctgaagagacccgattctctctcgtctgcact	2940
Db	2881	tgcagagacgctcgaagaccttgaaatctgaagatcggagacccgattctctctcgtctgcact	2940
Oy	2941	ggtctgcgtctgcagacccgtctgggcagagtgctctcctctctccctgggacatagtctctctgc	3000
Db	2941	ggtctgcgtctgcagacccgtctgggcagagtgctctcctctctccctgggacatagtctctctgc	3000
Oy	3001	ataaagaccccttcgacgctctcgttgtctctgtgaacacctccctgtatctctctgtgaaggg	3060
Db	3001	ataaagaccccttcgacgctctcgttgtctctgtgaacacctccctgtatctctctgtgaaggg	3060
Oy	3061	ggatctctgaagagggaaagagagcagagctctggagcagctgcagcccaaggggggtgtaggg	3120
Db	3061	ggatctctgaagagggaaagagagcagagctctggagcagctgcagcccaaggggggtgtaggg	3120
Oy	3121	ggacagagaaagcagagcagaaagctctgggtgctctccatcagctctcactatgatacgtctagactc	3180
Db	3121	ggacagagaaagcagagcagaaagctctgggtgctctccatcagctctcactatgatacgtctagactc	3180
Oy	3181	cagagcccgagagcccaatgtctctcagggaaagctcctaataccccaacagccacatttctct	3240
Db	3181	cagagcccgagagcccaatgtctctcagggaaagctcctaataccccaacagccacatttctct	3240
Oy	3241	tcccttaagcatatgaataatgtgcatttggccaataaacaagaaagatgcagaagctaaatgct	3300
Db	3241	tcccttaagcatatgaataatgtgcatttggccaataaacaagaaagatgcagaagctaaatgct	3300
Oy	3301	ggtacgctctctgcctgtgcattcaaaatctgggacagagcagatgagaaatgtgcagagatctg	3360
Db	3301	ggtacgctctctgtgcctgtgcattcaaaatctgggacagagcagatgagaaatgtgcagagatctg	3360
Oy	3361	ttaaaccttttcaacccttgacacccccaacgcagcttcagcagtgactgtcgtacagcacgg	3420
Db	3361	ttaaaccttttcaacccttgacacccccaacgcagcttcagcagtgactgtcgtacagcacgg	3420
Oy	3421	agtgacccggcagcggaggggggagaaagagagagagagtagtgatcttgagcaagaaag	3480
Db	3421	agtgacccggcagcggaggggggagaaagagagagagagtagtgatcttgagcaagaaag	3480

[illegible]

OY	4551	ataatattgaaacatctttctctgaagaaggtctcccaagttccaccaatgagttctctg	4650
Db	4561	atacatcttgaaaaaatcttctctgaagaaggtctcccaagttccaccaatgagttctctg	4620
OY	4621	catgcacacacacaggaatgaagaactatcttaagaagcttaacatctgaactgtgtcctga	4680
Db	4631	catgcacacacacaggaatgaagaactatcttaagaagcttaacatctgaactgtgtcctga	4680
OY	4681	tcgcaagactgaatctgaagaaggtctctcccaagaatacacagttctgtttaagaagctga	4740
Db	4681	tcgcaagactgaatctgaagaaggtctctcccaagaatacacagttctgtttaagaagctga	4740
OY	4741	aggaggaggaaatctgcgcctctctaagaatgtctccctcgagacctgtttaagggtc	4800
Db	4741	aggaggaggaaatctgcgcctctctaagaatgtctccctcgagacctgtttaagggtc	4800
OY	4801	cttggtcttcgcgcgcgtgttatcttctctgcgcctctgaagctttaaaggactgtctt	4860
Db	4801	cttggtcttcgcgcgcgtgttatcttctctgcgcctctgaagctttaaaggactgtctt	4860
OY	4861	ggatctccagttctccctgaagctgaagctctgcgcgcgcgcgcgcgcgcgcgcgcgcgc	4920
Db	4861	ggatctccagttctccctgaagctgaagctctgcgcgcgcgcgcgcgcgcgcgcgcgcgc	4920
OY	4921	tgaatggaataataaactagaataataatcctgtgtgaaatcagcacaccagtagtctcg	4980
Db	4921	tgaatggaataataaactagaataataatcctgtgtgaaatcagcacaccagtagtctcg	4980
OY	4981	tgtaatgt	5040
Db	4981	tgtaatgt	5040
OY	5041	taggaactatattgt	5100
Db	5041	taggaactatattgt	5100
OY	5101	caaacagactctcgtgaaggttatcttctctaagaactctgtctgcgcgcgcgcgcgcgcgc	5160
Db	5101	caaacagactctcgtgaaggttatcttctctaagaactctgtctgcgcgcgcgcgcgcgcgc	5160
OY	5161	ccgtgtgcacagccccacacgcgcctctgaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgt	5220
Db	5161	ccgtgtgcacagccccacacgcgcctctgaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgt	5220
OY	5221	gtctcccgatataataaacctctctcgtgaagctcgtgcgcgcgcgcgcgcgcgcgcgcgc	5280
Db	5221	gtctcccgatataataaacctctctcgtgaagctcgtgcgcgcgcgcgcgcgcgcgcgcgc	5280
OY	5281	caggcacctctcagcacagc	5300
Db	5281	caggcacctctcagcacagc	5300
RESULT 6			
ID	V51367	standard; DNA: 5300 BP.	
XX	V51367;		
AC			
XX	27-Oct-1998	(first entry)	
XX			
DE	Human TIGR promoter variant TIGRsv1 DNA.		
XX			
KW	TIGR: tribeocular meshwork induced glucocorticoid response protein; human;		
XX	diagnosis: glaucoma; polymorphism; steroid sensitivity; mutant; ss.		
OS	Homo sapiens.		
XX	Synthetic.		
XX			
PH	Key	location/Qualifiers	
FT	mutation	4406	
FT	/*tag= a	/note= "Wild-type A is replaced by G"	

Db 1621 taattcagggatctcttggaatgggaatggtgcataagagctgctcctagctccagac 1680
Oy 1681 cactggtccctcaactctctctccctcatcctcatcttaaggctaaagttaactttat 1740
Db 1681 cactggtccctcaactctctctccctcaactctcaactctcaagctaaagttaactttat 1740
Oy 1741 caacatgctcttggttaagagctcccaactcgttactgtaataaagatatacaataaag 1800
Db 1741 caacatgctcttggttaagagctcccaactcgttactgtaataaagatatacaataaag 1800
Oy 1801 ttcgaattggggacacatctgtgtgtgtataaggagagagacataccccagactcct 1860
Db 1801 ttcgaattggggacacatctgtgtgtgtataaggagagagacataccccagactcct 1860
Oy 1861 tgaagccccccggacagaggttctctctccagctggggagacccctgcagagacccgggtcc 1920
Db 1861 tgaagccccccggacagaggttctctctccagctggggagacccctgcagagacccgggtcc 1920
Oy 1921 tgggtgtccctggagcaaacctgcagacccgtgcacatggtgtgtttgtatcaactcttag 1980
Db 1921 tgggtgtccctggagcaaacctgcagacccgtgcacatggtgtgtttgtatcaactcttag 1980
Oy 1981 gaacgtgtgtcttcaatctctgtgtgactcgttcaatctcaagacatacatgtgaact 2040
Db 1981 gaacgtgtgtcttcaatctctgtgtgactcgttcaatctcaagacatacatgtgaact 2040
Oy 2041 tatgtagtaactatatactctgcagacacacagagacaaatctgtgagtaaaagcactctc 2100
Db 2041 tatgtagtaactatatactctgcagacacacagagacaaatctgtgagtaaaagcactctc 2100
Oy 2101 cctaacctctgtggaggtgagacgttctcaatggagagacgtgcagaaataataatagca 2160
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Oy 2281 cccccaagcccgagctcttccaaagcctccctccatcagttcaagacgtgcagctgacct 2340
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Oy 2341 gctctgctctccgtgaaatctgctgtgtgactgagctgagagactcctgtgctcagagct 2400
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Oy 2581 gctggcccaatgttcaatgtgttctcaaggggctggaggttctccgttctcctgtgagac 2640
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Oy 2641 cttttatcttctctcctgtctggagagagaaagctatattcaatgaagaagctgaatttc 2700
Db 2641 cttttatcttctctcctgtctggagagagaaagctatattcaatgaagaagctgaatttc 2700
Oy 2701 ataaagctagagctgttaaaatctccagaggtgtgacatgggttctcctcaagagggcttat 2760
Db 2701 ataaagctagagctgttaaaatctccagaggtgtgacatgggttctcctcaagagggcttat 2760

Oy 2761 ttaactgggaataagaagcgagctcatcttccctagagccgttaattcacggaaaggtgac 2820
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Oy 2821 tggagctcttcttcaatgtctctctggacaaactactcaagccctgtgtgagctgtctta 2880
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Db 2881 tgcagaagcgttgcgaataaccttggaaatcaggaatcccggtttcttctctggttctgcaat 2940
Oy 2941 ggttgctgtgcagacgtggagcaatgtctctctccctccctgggacataagctctctgct 3000
Db 2941 ggttgctgtgcagacgtggagcaatgtctctctccctccctgggacataagctctctgct 3000
Oy 3001 ataaagacccctgcagctctcgttctgttgcataacactccctgtgattctctgtgaggg 3060
Db 3001 ataaagacccctgcagctctcgttctgttgcataacactccctgtgattctctgtgaggg 3060
Oy 3061 ggaatttgagagggagagagagagagagagctggagcagctgagccacagaggggtgaggg 3120
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Oy 3121 ggaacaggaagcagagcagagagctgggtgtccatcagctcctcaactgatacgtcagagactc 3180
Db 3121 ggaacaggaagcagagcagagagctgggtgtccatcagctcctcaactgatacgtcagagactc 3180
Oy 3181 cagagccggagagccaaatgtcttcaggaagaagctcaatgaacccaacagccacatcttcc 3240
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Oy 3301 ggttagcttctgtcgtgcattcaaaaacttgggccaagagcaggtgagaaatgccaagagatg 3360
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Oy 3541 gttctagagagcagggctataatgttggggggaataaatcaagttcaagggagctgggaga 3600
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Oy 3781 taaagccaaacagattccaagcctaagttctgtgtgctatataatgtgtttttgaaataat 3840
Db 3781 taaagccaaacagattccaagcctaagttctgtgtgctatataatgtgtttttgaaataat 3840

OY	3841	ca	ttc	cag	cga	tgt	ttc	tca	tct	cga	tac	gaa	aag	atg	agc	tga	cct	tgt	tca	gct	3900
Db	3841	ca	ttc	cag	cga	tgt	ttc	tca	tct	cga	tac	gaa	aag	atg	agc	tga	cct	tgt	tca	gct	3900
OY	3901	ta	aa	ca	aa	c	ac	cc	ca	tt	c	tg	ta	aa	g	tt	c	ca	ag	tt	3960
Db	3901	ta	aa	ca	aa	c	ac	cc	ca	tt	c	tg	ta	aa	g	tt	c	ca	ag	tt	3960
OY	3961	aa	ga	a	t	ga	a	ac	t	tc	t	a	g	a	a	a	a	a	a	a	4020
Db	3961	aa	ga	a	t	ga	a	ac	t	tc	t	a	g	a	a	a	a	a	a	a	4020
OY	4021	ag	tt	g	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	4080
Db	4021	ag	tt	g	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	4080
OY	4081	t	g	c	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	4140
Db	4081	t	g	c	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	4140
OY	4141	t	t	a	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	4200
Db	4141	t	t	a	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	4200
OY	4201	g	a	t	a	t	a	a	a	a	a	a	a	a	a	a	a	a	a	a	4260
Db	4201	g	a	t	a	t	a	a	a	a	a	a	a	a	a	a	a	a	a	a	4260
OY	4261	t	g	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	4320
Db	4261	t	g	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	4320
OY	4321	c	t	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	4380
Db	4321	c	t	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	4380
OY	4381	t	t	a	a	c	a	t	a	a	a	a	a	a	a	a	a	a	a	a	4440
Db	4381	t	t	a	a	c	a	t	a	a	a	a	a	a	a	a	a	a	a	a	4440
OY	4441	c	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	4500
Db	4441	c	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	4500
OY	4501	a	t	t	c	t	g	a	a	a	a	a	a	a	a	a	a	a	a	a	4560
Db	4501	a	t	t	c	t	g	a	a	a	a	a	a	a	a	a	a	a	a	a	4560
OY	4561	a	t	a	a	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	4620
Db	4561	a	t	a	a	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	4620
OY	4621	c	a	t	t	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	4680
Db	4621	c	a	t	t	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	4680
OY	4681	t	g	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	4740
Db	4681	t	g	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	4740
OY	4741	a	g	g	g	g	g	a	a	a	a	a	a	a	a	a	a	a	a	a	4800
Db	4741	a	g	g	g	g	g	a	a	a	a	a	a	a	a	a	a	a	a	a	4800
OY	4801	c	t	t	t																

[illegible]

CC response in the patient and can be diagnostic of glaucoma or steroid
CC sensitivity. Base substitutions and base additions upstream of and within
CC TIGR exons can also be used to diagnose glaucoma.

XX Sequence 5304 BP; 1482 A; 1152 C; 1237 G; 1433 T; 0 other:

Query Match 99.7%; Score 5286; DB 19; Length 5304;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5300; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 atcttcttcagtttaccacagggtactatgaataatgaatgaataacaaatgtgaaag 60
DB 1 atcttcttcagtttaccacagggtactatgaataatgaatgaataacaaatgtgaaag 60
QY 61 tctctataactctatagctcccatctcgatgatatgtctttggcagggtatgaataatca 120
DB 61 tctctataactctatagctcccatctcgatgatatgtctttggcagggtatgaataatca 120
QY 121 ggaagaaaggagttaccagtttaagccaagtctccagagctgtctgtctctcttaattagtga 180
DB 121 ggaagaaaggagttaccagtttaagccaagtctccagagctgtctgtctctcttaattagtga 180
QY 181 cagaatgtctctctgacagaagaagctatctctcaaggaaacatcacatccaataggtaaatc 240
DB 181 cagaatgtctctctgacagaagaagctatctctcaaggaaacatcacatccaataggtaaatc 240
QY 241 catcaaaacagagcttaagaaacaggaatgagatgagctgacattggcccaaggaaatgtccag 300
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QY 481 aaacgctcaaaagcaatgatactccagatcccaaaagtgaattattttaaaacccagat 540
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DB 1861 tgaagcccccggagaggttctctctccacagctggggagagccctcgcaagcccggggtcc 1920
QY 1921 tgggtgtctctgaacaaactctgcccagccgtgtccactgtgttttgtatcatcctctag 1980
DB 1921 tgggtgtctctgaacaaactctgcccagccgtgtccactgtgttttgtatcatcctctag 1980
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[illegible]

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QY	3181	cagagccgagggccacaatctctccagaaagcgccaatgaaaccacagccacatcttcc	3240
Db	3181	cagagccgagggccacaatctctccagaaagcgccaatgaaaccacagccacatcttcc	3240
QY	3241	tcacctaaagcatalagacaaatggtcattctgcacataaccacaaagaaatgcagagactaa	3300
Db	3241	tcacctaaagcatalagacaaatggtcattctgcacataaccacaaagaaatgcagagactaa	3300
QY	3301	ggttagcttcttgcctcggaatcccaaaactctggccagagcgcaagtgggaaatgtccagagat	3360
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QY	3361	ttaaacctttcaacctctgacacagccccacagcgagccacagtgacctgtctgacacag	3420
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QY	4081	tgtccaaagggcaatcatattccaagtgtcctaaagtctac	4140
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Db	121	ggaagaaagagatcaccagtttaagcagaatggtccaaagctgtgtccatgtctcttaatttaatgta	180
Oy	181	cagatgtgtctctctgtacagaagaactattcttcaggaacaatccatccaatatgtgtaatc	240
Db	181	cagatgtgtctctctgtacagaagaagaactattcttcaggaacaatccatccaatatgtgtaatc	240
Oy	241	catacaacaggaagcttaagaaacagaaatgaaatggaagcattcccaagaaataatgacag	300
Db	241	catacaacaggaagcttaagaaacagaaatgaaatggaagcattcccaagaaataatgacag	300
Oy	301	gagagacaaataatgataaaaaataaactttttcccttgtttttaatttcagagaaaaaagt	360
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Oy	841	ggagaccctgagcattgtgccttaaggaagcgaatttcttaaggaatcctaagaactc	900
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Oy	901	ttgaaaggtccttgaaattttaaccattttaagtaataaagaataatgagatgtgaataacag	960
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Oy	1021	ggataggtcagaaataatcattgaagaatcactgtgtcccatcctaacttttcagaatgtac	1080
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Oy	1081	tgctatagccttcacacacagcgcccgatgtgtctgtcctaacaacacatctacaaccaa	1140
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Oy	1141	gtgcctcaaacattgtttaagctgtcatcctagtaggtcccatatcaaaatgccaacctccc	1200
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Db	2341	gctcgcgtcccgctgaatctgcctctgctgcacatctgcagctcgcgaagaccctctgcctcagcgt	2400
Oy	2401	ccagaagaagaaatcgagagaggaactagctctaaacggagaaatctcgagagggagacagtctctc	2460
Db	2401	ccagaagaagaaatcgagagaggaactagctctaaacggagaaatctcgagagggagacagtctctc	2460
Oy	2461	ccccaaagggaaagggggcccccacgtcccaaggaaatcccaaggaggtcgaggagaccgcagggag	2520
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Oy	2521	tcggagaccgtcgagctcgagccggctgcgcgaagagccaggaagcgtaaaagggcgaagctgaa	2580
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Db 5280 ccaagcaactctcagcaagc 5300
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RESULT 9
ID 237968 standard; DNA: 2800 BP.
AC 237968:
XX
XX 07-FEB-2000 (first entry)
DE Human GLC1A gene exon 1 and flanking sequences.
XX
XX GLC1A gene: PCR amplification: primary open wide angle glaucoma:
KM GLC1A gene: exon: human: ss.
XX
OS Homo sapiens.
XX
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PN W09951779-A2.
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XX 14-OCT-1999.
PD
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PF 07-APR-1999; 99WO-US07671.
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PR
XX (IOWA ) UNIV IOWA RES FOUND.
PA
XX
PI Stone EM, Sheffield VC, Alward WM, Fingert J;
XX
XX WPI: 2000-022956/02.
DR
XX
XX Determination of a predisposition to glaucoma by analysing mutations in
PT the GLC1A gene -
XX
PS Disclosure: Fig 1A: 137pp; English.
XX
XX The invention relates to a method for the determination of a
CC predisposition to glaucoma. The method comprises amplifying a GLC1A gene
CC with a primer pair selected from the sequences shown in 237981-238008.
CC The primers are used to determine whether a subject has or has the
CC potential to develop primary open wide angle glaucoma. The present
CC sequence represents the human GLC1A gene exon 1 and flanking sequences.
XX
XX Sequence 2800 BP: 781 A; 588 C; 673 G; 758 T; 0 other:
SQ

Query Match 35.1%; Score 1858; DB 21: Length 2800;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1869; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Oy 3431 agcgcaggggagagagaagaaagagagagatagtgtaagcaagaagacagatctcat 3490
    |||
Db 1 agcgcaggggagagagaag aaaaagagagagatagtgtaagcaagaagacagatctcat 59
Oy 3491 tcaaggcgagctgggaattgacacagggatataagtcacagtgatcctggtctcagaag 3550
    |||
Db 60 tcaaggcgagctgggaattgacacagggatataagtcacagtgatcctggtctcagaag 119
Oy 3551 gcaaggctctatctgtgggggggaaaaaatcagttcagggaagtcggggaacctgttctc 3610
    |||
Db 120 gcaaggctctatctgtgggggggaaaaaatcagttcagggaagtcggggaacctgttctc 179
Oy 3611 aatactatactttctccttacaagctggaatattctggaagtcacacagtgtaacctg 3670
    |||
Db 180 aatactatactttctccttacaagctggaatattctggaagtcacacagtgtaacctg 239
Oy 3671 aggcctgtaagatctagttctccttattaggaactctttctctgtggaattagca 3730
    |||
Db 240 aggcctgtaagatctagttctccttattaggaactctttctctgtggaattagca 299
Oy 3731 gcacaaggcgcaatcccggttctcttaacagagaagaagaacatctccaaagtaagccaa 3790
    |||
Db 300 gcacaaggcgcaatcccggttctcttaacagagaagaagaacatctccaaagtaagccaa 359
Oy 3791 cagattcaagcctaggtctctgctgactataatgattggtctttttgaaaaatcatctcagcg 3850
    |||
Db 360 cagattcaagcctaggtctctgctgactataatgattggtctttttgaaaaatcatctcagcg 419
Oy 3851 atgttactactctgattcagaagaatgagactgtaacctttgttcagctgttaacaaca 3910
    |||
Db 420 atgttactactctgattcagaagaatgagactgtaacctttgttcagctgttaacaaca 479
Oy 3911 cccatttgtaaatgtctcaagtctcaggtcttaactctcagaacacaaatcaataagaataag 3970
    |||
Db 480 cccatttgtaaatgtctcaagtctcaggtcttaactctcagaacacaaatcaataagaataag 539
Oy 3971 tctttagaagcaacgtgtttctccactcgtgaggtgagctgcgcaggcgcaatttgagaa 4030
    |||
Db 540 tctttagaagcaacgtgtttctccactcgtgaggtgagctgcgcaggcgcaatttgagaa 599
```

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OY 4031 taattacttcacagatctgacacgtctgttggtaatttaacaacataaagttgtccaag 4090
|||||
DB 600 taattacttcacagatctgacacgtctgttggtaatttaacaacataaagttgtccaag 659
OY 4091 caattcatattcaaaatggccttaaaatctacttcgaacagtttggtaatttatttgctca 4150
660 caattcatattcaaaatggccttaaaatctacttcgaacagtttggtaatttatttgctca 719
OY 4151 tggcacttggccttctgttcttctcttcttgggttatttaagttaaaagcaggattata 4210
720 ttggcacttggccttctgttcttctcttcttgggttatttaagttaaaagcaggattata 779
OY 4211 cctacagatccagaagcctgtgaattgaatggagaaaaaattacattttgtgtttacc 4270
780 cctacagatccagaagcctgtgaattgaatggagaaaaaattacattttgtgtttacc 839
OY 4271 acccttcaactaaatttaacatttatttccattgcgaatagagccaataacaaagtgg 4330
840 acccttcaactaaatttaacatttatttccattgcgaatagagccaataacaaagtgg 899
OY 4331 taataacagtaacctgtgatttgcatttaacaaatagaataacacagacattttactata 4390
900 taataacagtaacctgtgatttgcatttaacaaatagaataacacagacattttactata 959
OY 4391 ttacagtttggcagaacgtgtgaatggaatattatatactcaaaacttgaatt 4450
960 ttacagtttggcagaacgtgtgaatggaatattatatactcaaaacttgaatt 1019
OY 4451 agacctcctgtgagatctgttcttaacataataaacaatgttaaaatttggat 4510
1020 agacctcctgtgagatctgttcttaacataataaacaatgttaaaatttggat 1079
OY 4511 ttggaataacataattcattatcatttcttcttcttcttgaatacattattatttga 4570
1080 ttggaataacataattcattatcatttcttcttcttgaatacattattatttga 1139
OY 4571 aaacaccttctctgagaagagttccccaagatttccacaataggttcttggcagacaca 4630
1140 aaacaccttctctgagaagagttccccaagatttccacaataggttcttggcagacaca 1199
OY 4631 cacagagtaagaacctgaatttagagagcctaacaattgagctgtgagaatgagactg 4690
1200 cacagagtaagaacctgaatttagagagcctaacaattgagctgtgagaatgagactg 1259
OY 4691 aaattgaaagttctcccaagaataacacagttgttttaaaagcagaggtgaggggga 4750
1260 aaattgaaagttctcccaagaataacacagttgttttaaaagcagaggtgaggggga 1319
OY 4751 tctgcgagctctctatagaagaatgctccctgagagcctgtgaggtgtgctgtgtct 4810
1320 tctgcgagctctctatagaagaatgctccctgagagcctgtgaggtgtgctgtgtct 1379
OY 4811 ggcctgcgtgtatttctctctgtccctgcacagctcttaaaagcctgttggatctccag 4870
1380 ggcctgcgtgtatttctctctgtccctgcacagctcttaaaagcctgttggatctccag 1439
OY 4871 tctcctagcatagtgctgtgacagctgacagttctcctaagtcttgcagagttgaatgga 4930
1440 tctcctagcatagtgctgtgacagctgacagttctcctaagtcttgcagagttgaatgga 1499
OY 4931 taataaactaaataatctcttcttgaatcagaacacacagtagtctctgtgtgaagtgt 4990
1500 taataaactaaataatctctcttgaatcagaacacacagtagtctctgtgtgaagtgt 1559
OY 4991 tgaacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5050
1560 tgaacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1619
OY 5051 taattggggtatgggtgtgataaattgggagtctcttcttaaaagaatactccaaacagact 5110
1620 taattggggtatgggtgtgataaattgggagtctcttcttaaaagaatactccaaacagact 1679
OY 5111 tctgggaaggtatttcttaagaatctgtcgtgacagctggaaggaacccccctgtgtaca 5170
```

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DB 1680 tctgggaaggtatttcttaagaatctgtcgtgacagctgtgaaggaacccccctgtgtaca 1739
|||||
OY 5171 gccccacacagcctcaacgtgtgcacactctgtcttccccaatgaaggtgtgtcccaagt 5230
1740 gccccacacagcctcaacgtgtgcacactctgtcttccccaatgaaggtgtgtcccaagt 1799
OY 5231 atatataaacctctcgtgagctcgggacatgagccagacagccacacatccagacactc 5290
1800 atatataaacctctcgtgagctcgggacatgagccagacagccacacatccagacactc 1859
OY 5291 tcagcacagc 5300
1860 tcagcacagc 1869
DB 1860 tcagcacagc 1869

RESULT 10
O63862/c
ID O63862 standard; cDNA; 283 BP.
XX
AC O63862;
XX
DT 29-JAN-1995 (first entry)
XX
DE AP2 sequence obt'd. by PCR for tumour specific DNA.
XX
KW Arbitrary primers; AP-PCR; amplification; tumour cells; cancer;
KW insertions; deletions; ss.
XX
OS Synthetic.
XX
PN MO9411531-A.
XX
PD 26-MAY-1994.
XX
PE 12-NOV-1993; 93MO-US10904.
XX
PR 13-NOV-1992; 92US-0975737.
XX
PA (CALB-) CALIFORNIA INST BIOLOGICAL RES.
XX
PI Ionov Y, Malkhosyan S, Mccllelland M, pelnado MA;
PI Perucho M, WelshJ;
XX
DR WPI; 1994-183539/22.
XX
PT Identification of tumour cells - by analysing DNA to determine
PT whether insertions or deletions have occurred in reiterated
PT sequences
PS Disclosure; Page 52; 67pp; English.
XX
CC The sequence was obt'd. by PCR with arbitrary PCR primers used to
CC detect insertions or deletions in DNA sequences. Such mutations are
CC markers of cancer so such primers can be used in the diagnosis of
CC cancer, esp. colorectal, stomach or pancreatic tumours.
CC See also O63837-63.
XX
SO Sequence 283 BP; 63 A; 77 C; 94 G; 49 T; 0 other;

Query Match 3.3%; Score 176.4; DB 15; Length 283;
Best Local Similarity 80.4%; Pred.No.1.4e-31;
Matches 222; Conservative 0; Mismatches 46; Indels 8; Gaps 1;

OY 1281 gggctgagggctgtgtcttaacactaccgtatgctctacacctgagctcactgtcaact 1340
276 GACTCTCGCTCTGTCTGCCAGCGTGGAGTGCAATGGCGGATCTCGCTCACTGCAACT 217
DB 276 GACTCTCGCTCTGTCTGCCAGCGTGGAGTGCAATGGCGGATCTCGCTCACTGCAACT 217
OY 1341 ctgcctccacaggttcaagcaattctctgtctcagcctccgcgtagctggaactacag 1400
216 CCACCTCCCGGTTCAAGGATCTCTGCTCAGCTCCGAGTAGCTGGATTACAG 157
DB 216 CCACCTCCCGGTTCAAGGATCTCTGCTCAGCTCCGAGTAGCTGGATTACAG 157
```

OY 1401 CG-----caagccggcgctaaattttttatgtgtgagagaatgaggtttacacat 1452
 DB 156 CCGCGCGCCACACACCGCCGCTATTTTGTATTGATGAGACGGGGTTTACACCTGT 97
 OY 1453 tagccgcgcgtgtcttgaacctcctgaacctgaagtgatccaccacacctaagcctcctaag 1512
 DB 96 TGGCCAGCGCTGGTCTTGAACTCCTGTACCTCAGTGTGATCCACACACGTCGCTCCAAAG 37
 OY 1513 tgcctggattacagcatgaagtcacgcggcgccggcc 1548
 DB 36 TCGTGGATTACAGGTGTGAGCCACACCGCCAGCC 1

 RESULT 11
 ID 286967/c
 XX 286967 standard; DNA: 162450 BP.
 AC 286967:
 XX
 DT 16-MAY-2000 (first entry)
 XX
 DE Retinoblastoma binding protein-7 genomic DNA sequence.
 KM RBP-7; retinoblastoma binding protein-7; abnormal cell proliferation;
 KW diagnosis; therapy; cell differentiation; thyroid hyperplasia; psoriasis;
 KW benign prostate hypertrophy; cancer; sarcoma; neoplasm; leukaemia;
 KW lymphoma; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200000607-A1.
 PD 06-JAN-2000.
 XX
 PF 30-JUN-1999; 99WO-1B01242.
 XX
 PR 30-JUN-1998; 98US-009315.
 PR 10-DEC-1998; 98US-0111909.
 XX
 PA (GEST) GENSET.
 PI Bougueleret L;
 DR WPI: 2000-117170/10.
 XX
 PT Novel nucleic acid and polymorphic markers used for diagnosis of
 PT diseases, especially those involving abnormal cell proliferation and
 PT differentiation -
 XX
 PS Claim 1; Page 118-163; 223pp; English.
 XX
 This sequence represents the retinoblastoma binding protein-7 (RBP-7)
 genomic sequence of the invention. The RBP-7 coding sequence and
 regulatory sequences are useful for the recombinant production of the
 protein and for expressing heterologous nucleic acids. Primers and probes
 derived from the RBP-7 nucleotide sequence (e.g. 287035-287099) are
 useful for DNA amplification and detection methods. RBP-7 biallelic
 markers (see 286967) are useful for diagnosis of disease related
 to alteration in the regulation or in the coding regions of the RBP-7
 gene and for prognosis/diagnosis of an eventual treatment with
 therapeutic agents, especially agents acting on pathologies involving
 abnormal cell proliferation and/or differentiation, these include
 thyroid hyperplasia, psoriasis, benign prostate hypertrophy, cancers,
 including breast cancer, sarcoma and other neoplasms, bladder cancer,
 colon cancer, lung cancer, prostate cancer, various leukaemias, and
 lymphomas. RBP-7 antibodies are useful as diagnostic agents.

[illegible]

RESULT	12	
DE	T62346/C	
ID	T62346 standard; DNA; 282 BP.	
XX		
AC	T62346;	
XX		
DT	11-JUN-1997 (first entry)	
XX		
DE	Consensus Alu repeat sequence.	
XX		
KW	Bubble: interspersed repetitive element; ligation; annealing; primer;	
KW	PCR: polymerase chain reaction; amplification; chromosomal aberration;	
KW	genetic disorder; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	primer_bind	22..45
FT		/*tag- a
FT		/note= "binds primer 47-23 (T62347)"
FT	primer_bind	216..236
FT		/*tag- b
FT		/note= "binds either primer Alu-S (T62348) or
FT		Alu-J (T62349)"
FT	primer_bind	263..282
FT		/*tag- C
FT		/note= "binds primer Alu-end (T62350)"
XX		
PN	US5597694-A.	
XX		
PD	28-JAN-1997.	
XX		
PF	07-OCT-1993;	93US-0133629.
XX		
PR	07-OCT-1993;	93US-0133629.
XX		
PA	(MASI) MASSACHUSETTS INST TECHNOLOGY.	
XX		
PI	Housman DE, Munroe DJ;	
XX		
DR	WPI; 1997-108321/10.	
XX		
XX		
PT	Amplification of nucleic acid having interspersed repetitive element	
PT	- using bubble oligo:nucleotide	
XX		
PS	Disclosure; Column 19-20; 16pp; English.	
XX		
CC	The invention relates to the amplification of region of DNA containing	
CC	interspersed repetitive elements (IRE) such as the Alu repeat sequence	
CC	presented here. The method involves ligating a double stranded DNA	
CC	structure with a non-complementary region, a 'bubble', in the	

CC amplified by the primer pair R14B264/O560mak (T42806-7). The primers
CC also simultaneously amplify the loci Q900 (T42808) and Q120 (T42810).
CC The primers can be used for gene mapping, to assess paternity, maternity
CC and identity of children or in forensic science. In particular, they can
CC be used for the DNA fingerprinting identification of genetically related
CC or unrelated individuals.

XX
SQ Sequence 452 BP; 149 A; 92 C; 106 G; 85 T; 20 other;

Query Match 3.3%; Score 172.8; DB 17; Length 452;

Best Local Similarity 86.4%; Pred. No. 1.2e-30;

Matches 204; Conservative 1; Mismatches 23; Indels 8; Gaps 1;

Qy 1321 acctgagctcactgcaaacctctgctcccaaggttcaagcaattcctctgctcagcctcc 1380
Db 312 attctagctactgcaaacctctgctcccaaggttcaagcaattcctctgctcagcctcc 253
Qy 1381 cgcgtagctggaactacagcg-----cagcccgctaatlttctatgtagta 1432
Db 252 cgartagctcggaattacagctgccccgacacatgccccgctaatTTTGTATTTTAGTA 193
Qy 1433 gagaatggggttcaacataltacgcccgtgctcttgaactcctgacctcaggtgatcca 1492
Db 192 gagacggggtttcacacgttggtgacagctggtctcaaaactcctgacctcaggtgatctg 133
Qy 1493 cccacctcagcctcctcaaatgtctggaattacagggcaltgagtcacggccggccggcc 1548
Db 132 cccgctcagcctcctcaaatgtctggaattacagggcaltgagtcacggccggccggcc 77

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